

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 08/958,570

Source: _____

Date Processed by STIC: _____

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IFW16

RAW SEQUENCE LISTING

DATE: 12/21/2004

PATENT APPLICATION: US/08/958,570B

TIME: 10:39:06

Input Set : N:\CrF3\RULE60\08958570b.raw.txt

Output Set: N:\CRF4\12212004\H958570B.raw

SEQUENCE LISTING

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1 (1) GENERAL INFORMATION:
2   (i) APPLICANT: Gregory, Richard J.
3           Wills, Ken N.
4           Maneval, Daniel C.
5   (ii) TITLE OF INVENTION: Recombinant Adenoviral Vector and
6           Methods of Use
7   (iii) NUMBER OF SEQUENCES: 9
8   (iv) CORRESPONDENCE ADDRESS:
9           (A) ADDRESSEE: Townsend and Townsend and Crew LLP
10          (B) STREET: Two Embarcadero Center, Eighth Floor
11          (C) CITY: San Francisco
12          (D) STATE: California
13          (E) COUNTRY: USA
14          (F) ZIP: 94111-3834
15   (v) COMPUTER READABLE FORM:
16          (A) MEDIUM TYPE: Floppy disk
17          (B) COMPUTER: IBM PC compatible
18          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
19          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
20   (vi) CURRENT APPLICATION DATA:
C--> 21   (A) APPLICATION NUMBER: US/08/958,570B
C--> 22   (B) FILING DATE: 28-Oct-1997
23   (C) CLASSIFICATION:
24   (vii) PRIOR APPLICATION DATA:
W--> 25   (A) APPLICATION NUMBER: US/08/328,673
26   (B) FILING DATE: 25-Oct-1994
W--> 27   (A) APPLICATION NUMBER: US 08/142,669
28   (B) FILING DATE: 25-OCT-1993
W--> 29   (A) APPLICATION NUMBER: US 08/233,669
30   (B) FILING DATE: 26-APR-1994
31   (viii) ATTORNEY/AGENT INFORMATION:
32   (A) NAME: Smith, Timothy S.
33   (B) REGISTRATION NUMBER: 35,367
34   (C) REFERENCE/DOCKET NUMBER: 016930-000920US
35   (ix) TELECOMMUNICATION INFORMATION:
36   (A) TELEPHONE: (415) 576-0200
37   (B) TELEFAX: (415) 576-0300
38 (2) INFORMATION FOR SEQ ID NO: 1:
39   (i) SEQUENCE CHARACTERISTICS:
40   (A) LENGTH: 25 base pairs
41   (B) TYPE: nucleic acid
42   (C) STRANDEDNESS: single

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43          (D) TOPOLOGY: linear
W--> 44      (ii) MOLECULE TYPE: DNA
45          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
46          CGCCACCGAG GGACCTGAGC GAGTC                                     25
48 (2) INFORMATION FOR SEQ ID NO: 2:
49      (i) SEQUENCE CHARACTERISTICS:
50          (A) LENGTH: 20 base pairs
51          (B) TYPE: nucleic acid
52          (C) STRANDEDNESS: single
53          (D) TOPOLOGY: linear
W--> 54      (ii) MOLECULE TYPE: DNA
55          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
56          TTCTGGGAAG GGACAGAAGA                                           20
58 (2) INFORMATION FOR SEQ ID NO: 3:
59      (i) SEQUENCE CHARACTERISTICS:
60          (A) LENGTH: 25 base pairs
61          (B) TYPE: nucleic acid
62          (C) STRANDEDNESS: single
63          (D) TOPOLOGY: linear
W--> 64      (ii) MOLECULE TYPE: DNA
65          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
66          CGCGCTAGCT CTGCCCAAAG GAGCT                                     25
68 (2) INFORMATION FOR SEQ ID NO: 4:
69      (i) SEQUENCE CHARACTERISTICS:
70          (A) LENGTH: 39 base pairs
71          (B) TYPE: nucleic acid
72          (C) STRANDEDNESS: single
73          (D) TOPOLOGY: linear
W--> 74      (ii) MOLECULE TYPE: DNA
75          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
76          CGCGGTACCC TCGAGTCTAG ATATTGCCAG TGGTGGGAAG                   39
78 (2) INFORMATION FOR SEQ ID NO: 5:
79      (i) SEQUENCE CHARACTERISTICS:
80          (A) LENGTH: 35 base pairs
81          (B) TYPE: nucleic acid
82          (C) STRANDEDNESS: single
83          (D) TOPOLOGY: linear
W--> 84      (ii) MOLECULE TYPE: DNA
85          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
86          CGTGCGGCCG CTGGAGGACT TTGAGGATGT CTGTC                       35
88 (2) INFORMATION FOR SEQ ID NO: 6:
89      (i) SEQUENCE CHARACTERISTICS:
90          (A) LENGTH: 33 base pairs
91          (B) TYPE: nucleic acid
92          (C) STRANDEDNESS: single
93          (D) TOPOLOGY: linear
W--> 94      (ii) MOLECULE TYPE: DNA
95          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
96          CGCTCTAGAG AGACCAGTTA GGAAGTTTTC GCA                         33

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98 (2) INFORMATION FOR SEQ ID NO: 7:

99 (i) SEQUENCE CHARACTERISTICS:

100 (A) LENGTH: 2995 base pairs

101 (B) TYPE: nucleic acid

102 (C) STRANDEDNESS: single

103 (D) TOPOLOGY: linear

104 (ii) MOLECULE TYPE: cDNA

105 (ix) FEATURE:

106 (A) NAME/KEY: CDS

107 (B) LOCATION: 139..2925

108 (D) OTHER INFORMATION: /product= "RB"

109 /note= "retinoblastoma tumor suppressor"

110 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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111 TTCCGGTTTT TCTCAGGGGA CGTTGAAATT ATTTTGTAA CGGGAGTCGG GAGAGGACGG      60
112 GGC GTGCCCC GCGTGC GCGC GCGTCGTCCT CCGCGCGCT CCTCCACAGC TCGCTGGCTC      120
113 CCGCCGCGGA AAGGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC      171
114                               Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala
115                               1           5           10
116 ACC GCC GCC GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC      219
117 Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro
118                               15           20           25
119 CCT CCT GAG GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT      267
120 Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro
121                               30           35           40
122 CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA      315
123 Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala
124                               45           50           55
125 TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG      363
126 Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp
127                               60           65           70           75
128 TTA ACT TGG GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT      411
129 Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr
130                               80           85           90
131 ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA      459
132 Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala
133                               95           100          105
134 GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC      507
135 Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn
136                               110          115          120
137 ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT      555
138 Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp
139                               125          130          135
140 ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT      603
141 Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr
142                               140          145          150          155
143 GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT      651
144 Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu
145                               160          165          170
146 ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT      699

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147	Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser	
148	175 180 185	
149	GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG	747
150	Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly	
151	190 195 200	
152	GAA GTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG	795
153	Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met	
154	205 210 215	
155	CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC	843
156	Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu	
157	220 225 230 235	
158	AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA	891
159	Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg	
160	240 245 250	
161	ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA	939
162	Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu	
163	255 260 265	
164	GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT	987
165	Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys	
166	270 275 280	
167	AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT	1035
168	Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe	
169	285 290 295	
170	ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA	1083
171	Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu	
172	300 305 310 315	
173	AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA	1131
174	Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu	
175	320 325 330	
176	GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT	1179
177	Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser	
178	335 340 345	
179	ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT	1227
180	Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp	
181	350 355 360	
182	GAA GAG GTG AAT GTA ATT CTT CCA CAC ACT CCA GTT AGG ACT GTT ATG	1275
183	Glu Glu Val Asn Val Ile Leu Pro His Thr Pro Val Arg Thr Val Met	
184	365 370 375	
185	AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA	1323
186	Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln	
187	380 385 390 395	
188	CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA	1371
189	Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro	
190	400 405 410	
191	AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA	1419
192	Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys	
193	415 420 425	
194	GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA	1467
195	Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser	

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12/21/04

VERIFICATION SUMMARY

DATE: 12/21/2004

PATENT APPLICATION: US/08/958,570B

TIME: 10:39:07

Input Set : N:\Crf3\RULE60\08958570b.raw.txt

Output Set: N:\CRF4\12212004\H958570B.raw

L:21 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:22 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:27 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1)(vii)
L:29 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1)(vii)
L:44 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:54 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=2
L:64 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:74 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4
L:84 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5
L:94 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6